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2

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/848,806

DATE: 05/16/2001
 TIME: 14:54:19

Input Set : A:\00786.389002.SEQLIST.TXT
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4 <110> APPLICANT: Sheen, Jen
 6 <120> TITLE OF INVENTION: Calcium Dependent Protein Kinase
 7 Polypeptides as Regulators of Plant Disease Resistance
 10 <130> FILE REFERENCE: 00786/389002
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/848,806
 C--> 12 <141> CURRENT FILING DATE: 2001-05-04
 12 <150> PRIOR APPLICATION NUMBER: US 60/201,925
 13 <151> PRIOR FILING DATE: 2000-05-05
 15 <160> NUMBER OF SEQ ID NOS: 4
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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 20 <211> LENGTH: 495
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Arabidopsis thaliana
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 29 Gly Gln Gly Gln Phe Gly Thr Thr Tyr Leu Cys Thr Glu Lys Ser Thr
 30 35 40 45
 31 Ser Ala Asn Tyr Ala Cys Lys Ser Ile Pro Lys Arg Lys Leu Val Cys
 32 50 55 60
 33 Arg Glu Asp Tyr Glu Asp Val Trp Arg Glu Ile Gln Ile Met His His
 34 65 70 75 80
 35 Leu Ser Glu His Pro Asn Val Val Arg Ile Lys Gly Thr Tyr Glu Asp
 36 85 90 95
 37 Ser Val Phe Val His Ile Val Met Glu Val Cys Glu Gly Gly Glu Leu
 38 100 105 110
 39 Phe Asp Arg Ile Val Ser Lys Gly His Phe Ser Glu Arg Glu Ala Val
 40 115 120 125
 41 Lys Leu Ile Lys Thr Ile Leu Gly Val Val Glu Ala Cys His Ser Leu
 42 130 135 140
 43 Gly Val Met His Arg Asp Leu Lys Pro Glu Asn Phe Leu Phe Asp Ser
 44 145 150 155 160
 45 Pro Lys Asp Asp Ala Lys Leu Lys Ala Thr Asp Phe Gly Leu Ser Val
 46 165 170 175
 47 Phe Tyr Lys Pro Gly Gln Tyr Leu Tyr Asp Val Val Gly Ser Pro Tyr
 48 180 185 190
 49 Tyr Val Ala Pro Glu Val Leu Lys Lys Cys Tyr Gly Pro Glu Ile Asp
 50 195 200 205
 51 Val Trp Ser Ala Gly Val Ile Leu Tyr Ile Leu Leu Ser Gly Val Pro
 52 210 215 220
 53 Pro Phe Trp Ala Glu Thr Glu Ser Gly Ile Phe Arg Gln Ile Leu Gln
 54 225 230 235 240
 55 Gly Lys Leu Asp Phe Lys Ser Asp Pro Trp Pro Thr Ile Ser Glu Ala
 56 245 250 255

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58          260          265          270
59 Ile Ser Ala His Glu Ala Leu Cys His Pro Trp Ile Val Asp Glu Gln
60          275          280          285
61 Ala Ala Pro Asp Lys Pro Leu Asp Pro Ala Val Leu Ser Arg Leu Lys
62          290          295          300
63 Gln Phe Ser Gln Met Asn Lys Ile Lys Lys Met Ala Leu Arg Val Ile
64 305          310          315          320
65 Ala Glu Arg Leu Ser Glu Glu Glu Ile Gly Gly Leu Lys Glu Leu Phe
66          325          330          335
67 Lys Met Ile Asp Thr Asp Asn Ser Gly Thr Ile Thr Phe Glu Glu Leu
68          340          345          350
69 Lys Ala Gly Leu Lys Arg Val Gly Ser Glu Leu Met Glu Ser Glu Ile
70          355          360          365
71 Lys Ser Leu Met Asp Ala Ala Asp Ile Asp Asn Ser Gly Thr Ile Asp
72          370          375          380
73 Tyr Gly Glu Phe Leu Ala Ala Thr Leu His Met Asn Lys Met Glu Arg
74 385          390          395          400
75 Glu Glu Ile Leu Val Ala Ala Phe Ser Asp Phe Asp Lys Asp Gly Ser
76          405          410          415
77 Gly Tyr Ile Thr Ile Asp Glu Leu Gln Ser Ala Cys Thr Glu Phe Gly
78          420          425          430
79 Leu Cys Asp Thr Pro Leu Asp Asp Met Ile Lys Glu Ile Asp Leu Asp
80          435          440          445
81 Asn Asp Gly Lys Ile Asp Phe Ser Glu Phe Thr Ala Met Met Arg Lys
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83 Gly Asp Gly Val Gly Arg Ser Arg Thr Met Met Lys Asn Leu Asn Phe
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91 <212> TYPE: DNA

92 <213> ORGANISM: Arabidopsis thaliana

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97 acaccacgat taagagatca ttacctctg ggaaaaaagc taggccaagg ccaatttgga 180
98 acaacctatc tctgcacaga gaaatcaacc tccgctaatt acgcctgcaa atcgatcccg 240
99 aagcgaaagc tcgtgtgtcg cgaggattac gaagatgtat ggcgtgagat tcagatcatg 300
100 catcatctct ctgagcatcc aaatgttgtt aggatcaaag ggacttatga agattcggtg 360
101 ttgtttcata ttgttatgga ggtttgtgaa ggtggtgagc tttttgatcg gattgtttct 420
102 aaaggtcatt ttagtgagcg tgaagctgtc aagcttatta agacgattct tgggtgtgtt 480
103 gaggccttgc attctcttgg tgttatgcat agagatctca aacctgagaa tttcttggtt 540
104 gatagtccta aagatgatgc taagcttaag gctaccgatt ttggtttgtc tgtcttctat 600
105 aagccaggac aatatttata tgacgtagtt ggaagtcctg actatgttgc accagaggtg 660
106 ctaaagaaat gttatggacc tgaaatagat gtgtggagtg ctggtgttat cctctacatt 720
107 ttactcagcg gtgttctctc cttctgggca gagactgagt ctggaatctt tagacagata 780
108 ttgcaaggga agttagattt caaatctgac ccgtggccta ctatctcaga agctgctaaa 840

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109 gatttgatct ataaaatgct cgaaaggagc cccaagaaac gcatttctgc tcatgaagcc 900
110 ttgtgtcacc catggattgt cgatgaacaa gcagcaccag acaagcctct tgatccagca 960
111 gtcttatctc gtctaaagca gttttctcaa atgaataaga ttaagaaaat ggcattacgg 1020
112 gtaattgctg agagactttc agaggaagaa attggaggtc tgaaggaatt gttcaagatg 1080
113 atagacacag acaacagcgg aacgattact tttgaagagc tcaaagcggg tttgaagaga 1140
114 gtcggatctg aactgatgga atcagaaatc aagtctctca tggatgcggc tgatatcgac 1200
115 aacagtggta caatagacta cggagaattc cttagcagca ccttacacat gaacaagatg 1260
116 gagagagagg agattctggt ggctgcattt tcggactttg acaaagacgg aagcggttat 1320
117 atcaccatcg atgagcttca gtcagcttgc acagagtttg gtctatgtga tacacctotg 1380
118 gacgacatga tcaaggagat tgatcttgac aatgacggga agatcgattt ctcgaggttt 1440
119 acagcaatga tgaggaaagg agatggagtt gggagaagca gaaccatgat gaagaacttg 1500
120 aacttcaaca ttgctgatgc ttttggagtt gatggtgaaa aatctgatga ctgactcatc 1560
121 attcttccac aatttctggt tttttctctt ttaatttcgt ttatattttg aattctaat 1620
122 tctaaggata caaaaatata ttctggcttg ttttttgctt tcctttttat ttttgtaacat 1680
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134 Glu Thr Pro Arg Leu Arg Asp His Tyr Leu Leu Gly Lys Lys Leu Gly
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136 Gln Gly Gln Phe Gly Thr Thr Tyr Leu Cys Thr Glu Lys Ser Ser Ser
137 35 40 45
138 Ala Asn Tyr Ala Cys Lys Ser Ile Pro Lys Arg Lys Leu Val Cys Arg
139 50 55 60
140 Glu Asp Tyr Glu Asp Val Trp Arg Glu Ile Gln Ile Met His His Leu
141 65 70 75 80
142 Ser Glu His Pro Asn Val Val Arg Ile Lys Gly Thr Tyr Glu Asp Ser
143 85 90 95
144 Val Phe Val His Ile Val Met Glu Val Cys Glu Gly Gly Glu Leu Phe
145 100 105 110
146 Asp Arg Ile Val Ser Lys Gly Cys Phe Ser Glu Arg Glu Ala Ala Lys
147 115 120 125
148 Leu Ile Lys Thr Ile Leu Gly Val Val Glu Ala Cys His Ser Leu Gly
149 130 135 140
150 Val Met His Arg Asp Leu Lys Pro Glu Asn Phe Leu Phe Asp Ser Pro
151 145 150 155 160
152 Ser Asp Asp Ala Lys Leu Lys Ala Thr Asp Phe Gly Leu Ser Val Phe
153 165 170 175
154 Tyr Lys Pro Gly Gln Tyr Leu Tyr Asp Val Val Gly Ser Pro Tyr Tyr
155 180 185 190
156 Val Ala Pro Glu Val Leu Lys Lys Cys Tyr Gly Pro Glu Ile Asp Val
157 195 200 205
158 Trp Ser Ala Gly Val Ile Leu Tyr Ile Leu Leu Ser Gly Val Pro Pro
159 210 215 220

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160 Phe Trp Ala Glu Thr Glu Ser Gly Ile Phe Arg Gln Ile Leu Gln Gly
161 225                230                235                240
162 Lys Ile Asp Phe Lys Ser Asp Pro Trp Pro Thr Ile Ser Glu Gly Ala
163                245                250                255
164 Lys Asp Leu Ile Tyr Lys Met Leu Asp Arg Ser Pro Lys Lys Arg Ile
165                260                265                270
166 Ser Ala His Glu Ala Leu Cys His Pro Trp Ile Val Asp Glu His Ala
167                275                280                285
168 Ala Pro Asp Lys Pro Leu Asp Pro Ala Val Leu Ser Arg Leu Lys Gln
169                290                295                300
170 Phe Ser Gln Met Asn Lys Ile Lys Lys Met Ala Leu Arg Val Ile Ala
171 305                310                315                320
172 Glu Arg Leu Ser Glu Glu Glu Ile Gly Gly Leu Lys Glu Leu Phe Lys
173                325                330                335
174 Met Ile Asp Thr Asp Asn Ser Gly Thr Ile Thr Phe Glu Glu Leu Lys
175                340                345                350
176 Ala Gly Leu Lys Arg Val Gly Ser Glu Leu Met Glu Ser Glu Ile Lys
177                355                360                365
178 Ser Leu Met Asp Ala Ala Asp Ile Asp Asn Ser Gly Thr Ile Asp Tyr
179                370                375                380
180 Gly Glu Phe Leu Ala Ala Thr Leu His Ile Asn Lys Met Glu Arg Glu
181 385                390                395                400
182 Glu Asn Leu Val Val Ala Phe Ser Tyr Phe Asp Lys Asp Gly Ser Gly
183                405                410                415
184 Tyr Ile Thr Ile Asp Glu Leu Gln Gln Ala Cys Thr Glu Phe Gly Leu
185                420                425                430
186 Cys Asp Thr Pro Leu Asp Asp Met Ile Lys Glu Ile Asp Leu Asp Asn
187                435                440                445
188 Asp Gly Lys Ile Asp Phe Ser Glu Phe Thr Ala Met Met Lys Lys Gly
189                450                455                460
190 Asp Gly Val Gly Arg Ser Arg Thr Met Arg Asn Asn Leu Asn Phe Asn
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192 Ile Ala Glu Ala Phe Gly Val Glu Asp Thr Ser Ser Thr Ala Lys Ser
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206 ctctgtacag agaaatcatc atcagcta atcagcttgca aatcaatccc aaaacgtaag 180
207 cttgtatgtc gtgaagacta cgaagatgta tggcgtgaga ttcagatcat gcatcatctc 240
208 tctgagcatc ctaatgttgt tagaatcaag ggtacttatg aagactctgt ttttgttcac 300
209 attgttatgg aagtttgtga aggtgtgag ctttttgatc ggattgtttc taaagggtgt 360
210 tttagtgaac gtgaagctgc taagttgatt aagactattc ttggtgttgt tgaggcttgt 420
211 cattctcttg gtgttatgca tagagatctt aagcctgaga atttcttgtt tgatagtccc 480

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212 agtgatgatg ctaagcttaa agctacagac tttggtttgt ctgtcttcta caagccaggg 540
213 cagtatctgt atgatgtagt tggaagtcg tattatgttg cacctgaggt tctgaagaaa 600
214 tgttatggac cagagataga cgtgtggagc gccggtgtta tcttgtagat cttactaagt 660
215 ggggttcctc ctttttgggc agaaaccgag tcaggaatct ttaggcagat attgcaaggg 720
216 aagatagatt ttaaactctga tccgtggcct actatctcag aaggtgctaa agatttgatt 780
217 tacaaaatgc tcgataggag ccccaagaaa cgtatttctg cacatgaagc attgtgtcac 840
218 ccttgattg ttgatgaaca tgctgcacca gacaagcctc tcgaccagc agtcttgctg 900
219 cgacttaagc agttctcgca aatgaataaa atcaagaaaa tggccttacg agtaatcgcg 960
220 gagagactct cggaggaaga gattggtggt ctgaaggaaat tggtcaaaat gatagataca 1020
221 gacaacagtg gaacaatcac ctttgaagag cttaaagcag gtctaaagag agttggatct 1080
222 gaattgatgg aatcagaaat caagtctctt atggatgcgg cggatataga caacagtggg 1140
223 acaatagact acggtgaatt cctagcagcg acattacata taaacaagat ggagagagaa 1200
224 gagaacttgg tggttgcggt ttcatacttt gataaagatg gtagcgggta tatcaccatt 1260
225 gacgagcttc aacaagcctg cacagagttt ggtctctgtg acactcctct tgatgacatg 1320
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227 atgaagaaag gagatggtgt tgggaggagc agaactatga ggaacaactt gaacttcaat 1440
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231 ttataagcat ggataatttt gcttcatatt ttctgcg 1657

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VERIFICATION SUMMARY

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Output Set: N:\CRF3\05162001\I848806.raw

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date